

**AMENDMENTS TO THE SPECIFICATION:**

**Page 8, line 4, insert the following text:**

SEQ ID NO: 25 is Region 1 of the corn monofunctional Aspartate kinase described in Example 8.

SEQ ID NO: 26 is the Region 1 of the E.coli monofunctional Aspartate kinase described in Example 8.

SEQ ID NO: 27 is the Region 2 in the corn monofunctional Aspartate kinase described in Example 8.

SEQ ID NO: 28 is the Region 2 in the E.coli monofunctional Aspartate kinase described in Example 8.

**Paragraph on page 11, line 20 through page 12, line 5:**

A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol.* 215:403-410; ~~see also www.ncbi.nlm.nih.gov/BLAST/~~). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches amino acid and nucleotide sequences encoding polypeptides that comprise one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

**Paragraph on page 26, lines 3-21:**

**EXAMPLE 2**

**Identification of cDNA Clones**

cDNA clones encoding aspartate kinase were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol.* 215:403-410; see also [www.ncbi.nlm.nih.gov/BLAST/](http://www.ncbi.nlm.nih.gov/BLAST/)) searches for similarity to sequences contained in the BLAST “nr” database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the “nr” database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the “nr” database using the BLASTX algorithm (Gish and States (1993) *Nat. Genet.* 3:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as “pLog” values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST “hit” represent homologous proteins.

**Paragraph on page 35, line 23 through page 36 line 4:**

A second method used PCR mutagenesis to create a site-specific mutation in the corn monofunctional aspartate kinase gene that reduces the encoded enzyme's sensitivity to inhibition by L-lysine. The particular amino acid substitutions to yield lysine-insensitive monofunctional corn aspartate kinase were based upon the homology that was discovered between monofunctional corn aspartate kinase and monofunctional *E. coli* aspartate kinase. Specifically, in two regions where particular amino acid substitutions were known to yield lysine-insensitive monofunctional *E. coli* aspartate kinase (see U.S. Patent 5,773,691) the monofunctional corn aspartate kinase was found to have similar amino acid sequence. These regions are shown below:

Region 1

monofunctional corn aspartate kinase TSEVSVSVD **(SEQ ID NO:25)**  
monofunctional *E. coli* aspartate kinase TSEVSVALTLD **(SEQ ID NO:26)**

The lysine-insensitive mutant monofunctional *E. coli* aspartate kinase has the underlined T (threonine) residue changed to I (isoleucine).

Region 2

monofunctional corn aspartate kinase    SSRMLGQYGFLA (SEQ ID NO:27)  
monofunctional *E. coli* aspartate kinase    SLNMLHSRGFLA (SEQ ID NO:28)

**AMENDMENTS TO THE SEQUENCE LISTING**

A substitute Sequence Listing is filed herewith. The Sequence Listing includes new SEQ ID NOs: 25-28.

Furthermore for clarification, nucleotides 29 to 1708 of SEQ ID NO:5 encode the 560 amino acid sequence of SEQ ID NO:6.